

SEQUENCE LISTING

SEQ ID 1 – *NadA* from strain 2996, with C-terminus deletion

1AP20 Rec'd 11/13/06 11/13/06 2006

MKHFP SKVLTTAILATFCSGALAAATNDDDVKKAATVAIAAAYNNGQEINGFKAGETIYDIDEDGTITKKDATAA
DVEADDFKGLGLKKVVTNLTCTVNENKQNVDAKVKAASEIEKLTTKLADTDAALADTDAALDATTNALNKLGE
5 NITTFAEETKTNIVKIDEKLEAVADTVDKHAEAFNDIADSLDETNTKADEAVKTANEAKQTAEETKQNVDAKVK
AAETAAGKAEAAAGTANTAADKAEVAAKVTDIKADIATNKDNIAKKANSADVTTREESDSKFVRIDGLNATTE
KLDTRLASAEKSIADHDTRLNGLDKTVSDLRKETRQGLAEQAALSGLFQPYNVG

SEQ ID 2 – *NadA* from strain 2996, with C-terminus deletion and leader peptide processed

ATNDDDVKKAATVAIAAAYNNGQEINGFKAGETIYDIDEDGTITKKDATAADVEADDFKGLGLKKVVTNLTCTV
10 NENKQNVDAKVKAASEIEKLTTKLADTDAALADTDAALDATTNALNKLGENITTFAEETKTNIVKIDEKLEAV
ADTVDKHAEAFNDIADSLDETNTKADEAVKTANEAKQTAEETKQNVDAKVKAASETAAGKAEAAAGTANTAADKA
EVAAKVTDIKADIATNKDNIAKKANSADVTTREESDSKFVRIDGLNATTEKLDTRLASAEKSIADHDTRLNGL
DKTVSDLRKETRQGLAEQAALSGLFQPYNVG

SEQ ID 3 – *AG741* from MC58 strain

VAADIGAGLADALTAPLDHKDKGLQSLTLDQSVRKNEKLKLAQAQAEKTYGNGDSLNTGKLKNDKVSRLFDFIRO
15 IEVDGQLITLESSEGFQVYKQSHSALTAFQTEQIQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPEGGGRATYRGT
AFGSDDAGGKLTYYTIDFAAQGNGKIEHLKSPELNVDLAAADIKPDGKRHAVISGSVLYNQAEEKSYSLGIFGG
KAQEVAGSAEVKTVNGIRHIGLAAKQ

SEQ ID 4 – 936 from MC58 strain with leader peptide processed

VSAVIGSAAVGAASAVDRRTTGAQTDDNVMALRIETTARSYLQNNQTKGYTPQISVVGYNRHLLLLGQVATEG
20 EKQFVGQIARSEQAAEGVYNYITVASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGIL
TPEEQAOITQKVSTTVGVQKVITLYQNYVQR

SEQ ID 5 – 953 from MC58 strain with leader peptide processed

ATYKVDEYHANARFAIDHFNSTNVGGFYGLTGSVEFDQAKRDGKIDITIPIANLQSGSQHFTDHLKSADIFDA
25 AQYPDIFRVSTKFNFGKKLVSDGNLTMHGKTAPVKLKAEKFENCYQSPMEKTEVCGGDFSTTIDRTKWGM DYL
VNVGMTKSVRIDIQIEAAKQ

SEQ ID 6 – *AG287* from MC58 strain

SPDVKSADTLSPAPVSEKETEAKEDAPQAGSQGQAPSQAQSQDMAAVSEENTGNGGAVTADNPKNEDVA
QNDMPQNAAGTDSSTPNHTPDPNMLAGNMENQATDAGESSQANQPDMANAADMGGDDPSAGGQNAAGTAAQ
30 ANQAGNNQAAGSSDPIPASNPAPANGGSNFRVLDLAVGLIDGPSQNTLTHCKGDCSGNNFLDEEVQLKSEF
EKLSADADKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKPKPTSFAFRRSARSRRSLPAEMPLIPVNQAD
TLIVDGEAVSLTGHSGNIFAPEGNYRYLTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRP
YPTRGRFAAKVDFGSKSVGDIIDSGDDLHMGTOQKFAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSY
RPTDAEKGFGVFAAGKEQD

SEQ ID 7 – 287-953 hybrid

MASPDVKSADTLSPAPVSEKETEAKEDAPQAGSQGQAPSQAQSQDMAAVSEENTGNGGAAATDKPKNEDE
GAQNDMPQNAADTDSLTPNHTPASNMPAGNMENQAPDAGESEQANQPDMANADGMGGDDPSAGGENAGNTAA
QGTNQAENNQTAGSQNPASSTNPSATNSGGDFGRNTVGNVVIDGPSQNTLTHCKGDCSGNNFLDEEVQLKS
EFEKLSADADKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKPKPTSFAFRRSARSRRSLPAEMPLI
40 PVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFH
TENGRPSPSRGRFAAKVDFGSKSVGDIIDSGDGLHMGTOQKFAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEV
AGKYSYRPTDAEKGFGVFAAGKEQDGGGGGATYKVDEYHANARFAIDHFNSTNVGGFYGLTGSVEFDQAKR

DGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNFNKGKLVSDGNLTMHGKTAPVKLKA EK
FNCYQSPMAKTEVCGGDFSTTIDRTKWGVDYLVNVMGKTSVRIDIQIEAAKQ*

SEQ ID 8 – 936-741 hybrid

5 MVS AVIGSAAVGA KSAVDRRTTGAQTDDNVMALRIETTARSYL RQNNQTKGYTPQISVVGYNRHL LLLGQVATE
GEKQFVGQIARSEQAAEGVYNYITVASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGI
LTPEEQAQITQKVSTTVGVQKVITLYQNYVQRSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVRKN
EKLKLAQAQGA EKTYGNGDSLNTGKLKNDKVS RFD FIRQIEVDGQLITLESGEFQVYKQSHSALTAFQTEQIQDS
EHSGK MVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSDDAGGKLT YTIDFAAKQGNKGIEHLKSP ELNV
DLAAADIKPDGKRHAVISGSVLYNQA EKGSYSLGIFGGKAQEVAGSAEVKTVNGIRHIGLA AKQ*

10 **SEQ ID 9 – linker**

GSGGGG

SEQ ID 10 – 741 sequence

15 CSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVRKN EKLKLAQAQGA EKTYGNGDSLNTGKLKNDKVS
RFD FIRQIEVDGQLITLESGEFQVYKQSHSALTAFQTEQIQDSEHSGK MVAKRQFRIGDIAGEHTSFDKLPEGG
RATYRGTAFGSDDAGGKLT YTIDFAAKQGNKGIEHLKSP ELNVDLAAADIKPDGKRHAVISGSVLYNQA EKGSY
SLGIFGGKAQEVAGSAEVKTVNGIRHIGLA AKQ

SEQ ID 11 – 741 sequence

20 CSSGGGGVAADIGAGLADALTAPLDHKDKSLQSLTLDQSVRKN EKLKLAQAQGA EKTYGNGDSLNTGKLKNDKVS
RFD FIRQIEVDGQLITLESGEFQIYKQDHS AVVALQIEKINNPDKIDSLINQRSFLVSGLGGEHTAFNQLPDGK
AEYHGKAFSSDDAGGKLT YTIDFAAKQGHGKIEHLKTP EQNVELAAAE LKADEKSHAVILGDTRYGSEEKGT YH
LALFGDRAQE IAGSATVKIG EKVHEIGIAGKQ

SEQ ID 12 – 741 sequence

25 CSSGGGGSGGGGVAADIGTGLADALTAPLDHKDKGLKSLTLED SIPQNGTLTLSAQGA EKTFKAGDKDNSLNTG
KLKNDKISRFDVQKIEVDGQTITLASGEFQIYKQNHSAVVALQIEKINNPDKTDSLINQRSFLVSGLGGEHTA
FNQLPGGKA EYHGKAFSSDDPNGR LHYSIDFTKKQGYGRIEHLKTL EQNVELAAAE LKADEKSHAVILGDTRYG
SEEKGT YHLALFGDRAQE IAGSATVKIG EKVHEIGIAGKQ